

CT Check Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Amino Acid Sequence

Arginine

Bacteriophages

Base Sequence

Circular Dichroism

Conserved Sequence

*Cytochrome b: BI, biosynthesis

*Cytochrome b: CH, chemistry

Databases, Factual

Enzyme-Linked Immunosorbent Assay

Genetic Vectors

Hemerythrin: AA, analogs & derivatives

Hemerythrin: BI, biosynthesis

Hemerythrin: CH, chemistry

Models, Structural

Molecular Sequence Data

Mutagenesis, Site-Directed

Oligodeoxyribonucleotides

Protein Folding

*Protein Structure, Secondary

Proteins: BI, biosynthesis

*Proteins: CH, chemistry

Random Allocation

Recombinant Proteins: BI, biosynthesis

Recombinant Proteins: CH, chemistry

Serine

Serum Albumin, Bovine

Tryptophan

RN 56-45-1 (Serine); 73-22-3 (Tryptophan); 74-79-3 (Arginine); 9035-37-4 (Cytochrome b); 9064-79-3 (cytochrome b562, E coli)

CN 0 (Genetic Vectors); 0 (Hemerythrin); 0 (Oligodeoxyribonucleotides); 0 (Proteins); 0 (Recombinant Proteins); 0 (Serum Albumin, Bovine); 0 (myohemerythrin)

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(FILE 'HOME' ENTERED AT 13:07:46 ON 09 JUL 2003)
SET COST OFF

FILE 'HCAPLUS' ENTERED AT 13:07:58 ON 09 JUL 2003

L1 1 S US20020048776/PN
L2 6 S (WO9726277 OR WO9116683 OR WO9321206 OR US5557535 OR WO930148
L3 1 S GOEDE ?/AU AND 1997/PY AND (18 AND 9 AND 1113)/SO

FILE 'WPIX' ENTERED AT 13:15:16 ON 09 JUL 2003

L4 6 S (WO9726277 OR US5495423 OR WO9116683 OR WO9321206 OR US555753

FILE 'MEDLINE' ENTERED AT 13:15:36 ON 09 JUL 2003

L5 1 S PREISSNER ?/AU AND 1998/PY AND (280 AND 3 AND 535)/SO

FILE 'WPIX' ENTERED AT 13:16:03 ON 09 JUL 2003

L6 1 S US20020048776/PN
E FROMMEL C/AU
L7 3 S E3
E PREISSNER R/AU
L8 3 S E3
E GOEDE A/AU
L9 4 S E3, E4
E JERINI/PA
L10 11 S E3-E7

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          E FROEMMEL/AU
L11      7 S E5
L12      1 S L4,L6 AND L7-L11
L13     18 S L7-L11 NOT L12
L14      7 S L4,L6,L12

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FILE 'WPIX' ENTERED AT 13:26:40 ON 09 JUL 2003

FILE 'HCAPLUS' ENTERED AT 13:26:57 ON 09 JUL 2003

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          E PREISSNER C/AU
          E PREISSNER R/AU
L15     18 S E3,E4
          E FROMMEL C/AU
L16     16 S E3,E5
          E FROEMMEL C/AU
L17     43 S E3,E4
          E GOEDE A/AU
L18     63 S E3-E6,E9,E10
          E JERINI/PA,CS
L19     36 S E3-E22
L20      2 S L1-L3 AND L15-L19
L21      8 S L1-L3,L20
L22    149 S L15-L19 NOT L21
          E LIGAND/CT
          E E38+ALL
L23    15338 S E1
L24    30095 S E1+NT
L25      1 S L21 AND L23,L24
L26      8 S L21,L25
L27      0 S L22 AND L23,L24
L28      5 S L22 AND LIGAND
          E PEISSNER R/AU
L29      1' S E4 AND L28
L30      5 S L28,L29
          SEL DN AN 4 5
L31      2 S L30 AND E1-E6
L32     10 S L26,L31
L33    343188 S L23,L24 OR LIGAND
L34    101010 S L33 AND (?PEPTIDE? OR ?PROTEIN? OR ENZYM? OR AMINO ACID?)
L35     21636 S L33 AND (PEPTIDE? OR PROTEIN? OR ENZYM? OR AMINO ACID?)/SX,SC
L36     48827 S L33 AND (PEPTIDE? OR PROTEIN? OR ENZYM? OR AMINO(L)ACID?)/CW
L37    103800 S L34-L36
          E SECONDARY STRUCTURE/CT
L38     6956 S E3,E4
          E E3+ALL
L39     24837 S E4,E3+NT
L40     1318 S L37 AND L38,L39
L41     1021 S L37 AND SECONDARY STRUCTURE
L42     1776 S L40,L41
          E E1+ALL
L43     21752 S E2,E3,E1+NT AND L37
L44     1601 S L42 AND L43
L45     1776 S L42,L44
          E MOLECULAR SURFACE/CT
          E E3+ALL
L46     367 S E3
          E E4+ALL
L47     322 S E2+NT
          E E5+ALL
L48     4867 S E2+NT
          E E15+ALL
          E MOLECULAR SURFACE/CT
          E E4+ALL

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L49      706 S E2
L50      14 S L45 AND (L46-L49 OR MOLECULAR SURFACE)
          SEL DN AN 3 6 10 11 14
L51      5 S L50 AND E1-E15
L52      32 S L45 AND (PROTEIN SURFACE OR SURFACE AREA)
L53      27 S L52 NOT L50
L54      1 S L53 AND PROTEIN SURFACE RECOGNITION
L55      6 S L51,L54
          E MOLECULAR RECOGNITION/CT
          E E3+ALL
L56      8689 S E2,E1+NT
          E E6+ALL
L57      80573 S E1+NT
          E E17+ALL
L58      4443 S E4,E3+NT
          E E15+ALL
L59      549 S E2
L60      359 S L45 AND L56-L59
L61      15 S L60 AND (DRUG SCREENING+NT OR SCREENING+NT OR HIGH THROUGHPUT
L62      11 S L60 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES
L63      18 S L61,L62
L64      3 S L32 AND L33-L63
L65      14 S L32,L55,L64
L66      9 S L65 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES
L67      14 S L65,L66
L68      35 S L45 AND (COMPUTER APPLICATION+NT OR ALGORITHM+NT OR DATABASES
          E MODEL/CT
          E E6+ALL
          E E2+ALL
          E E2+ALL
L69      179 S L45 AND E3-E5,E2+NT
L70      25 S L45 AND E39+NT
L71      16 S L45 AND E41+NT
          E MODEL/CT
          E E6+ALL
          E E2+ALL
L72      208 S L68-L71
L73      22 S L72 AND LIGAND?/CW
L74      34 S L67,L73
L75      23 S L72 AND L74
L76      34 S L74,L75
L77      21 S L76 AND (PY<=1999 OR PRY<=1999 OR AY<=1999)
L78      13 S L76 NOT L77
L79      87 S L72 AND (PY<=1999 OR PRY<=1999 OR AY<=1999)
L80      76 S L79 NOT L77
          SEL DN AN 2 23 41 74 75
L81      5 S L80 AND E1-E15
L82      26 S L77,L81
L83      26 S L82 AND L1-L3,L15-L82
L84      26 S L83 AND (SCREEN? OR SECOND? OR STRUCTUR? OR MOLECUL? OR SURFA
L85      23 S L84 AND (AMINO ACID OR CONFORM? OR FOLD?)
L86      26 S L84,L85

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FILE 'HCAPLUS' ENTERED AT 14:16:12 ON 09 JUL 2003

FILE 'MEDLINE' ENTERED AT 14:16:42 ON 09 JUL 2003

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          E PROTEIN STRUCTURE/CT
          E E12+ALL
L87      32663 S E10+NT
          E DATABASE/CT
          E E35+ALL
L88      815 S E6+NT AND L87
L89      410 S L88 AND PY<=1999

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L90 19542 S L87 AND PY<=1999
L91 14192 S L1./CT AND L90
L92 14192 S L89,L91
E MOLECULAR SURFACE/CT
E E1+ALL
L93 13229 S E8+NT AND L92
E E80+ALL
L94 4712 S E4+NT AND L92
L95 1044 S LIGAND AND L92
L96 1018 S L95 AND L93,L94
E LIGANDS/CT
E E3+ALL
L97 476 S E7 AND L90
L98 1440 S LIGAND AND L90
L99 1440 S L97,L98,L95
L100 1359 S L99 AND D12./CT
L101 536 S L99 AND D8./CT
L102 1433 S L100,L101
E CONFORMATION/CT
E E8+ALL
L103 1433 S L102 AND E2+NT
E E2+ALL
L104 13 S L103 AND L88
SEL DN AN 1 5 7 8 9 11-13
L105 8 S L104 AND E1-E24
E BINDING SITES/CT
E E3+ALL
L106 172215 S E4+NT
E E26+ALL
L107 105279 S E7+NT
L108 5586 S L90 AND L106,L107
L109 809 S L108 AND L99
L110 7 S L109 AND L88
L111 594 S L109 AND L93,L94
L112 805 S L109 AND L103
L113 10 S L105,L110 AND L87-L112
E FROMMEL C/AU
L114 45 S E3,E4
E FROEMMEL C/AU
L115 3 S E3,E4
E PREISSNER R/AU
L116 14 S E3,E4
E GOEDE A/AU
L117 18 S E3-E8
L118 64 S L114-L117
L119 17 S L118 AND L87-L113
SEL DN AN 2-5 8 10-12
L120 8 S E1-E24
L121 17 S L113,L120 AND L87-L120
L122 56 S L118 NOT L121
SEL DN AN 14 22
L123 3 S E24-E30
L124 19 S L121,L123 AND L87-L123
L125 19 S L5,L124

FILE 'MEDLINE' ENTERED AT 14:34:11 ON 09 JUL 2003